

**AMENDMENT**

Please amend the application without prejudice, without admission, without surrender of subject matter, and without any intention of creating any estoppel as to equivalents, as follows.

**In the Specification**

Please amend the paragraph beginning at page 48, line 1, as follows:

-- Further homologues of known mammalian Notch ligands may be identified using standard techniques. By a "homologue" it is meant a gene product that exhibits sequence homology, either amino acid or nucleic acid sequence homology, to any one of the known Notch ligands, for example as mentioned above. Typically, a homologue of a known Notch ligand will be at least 20%, preferably at least 30%, identical at the amino acid level to the corresponding known Notch ligand. Techniques and software for calculating sequence homology between two or more amino acid or nucleic acid sequences are well known in the art (see for example the National Center for Biotechnology Information website, maintained by the National Institutes of Health and the National Library of Medicine, <http://www.ncbi.nlm.nih.gov> and Ausubel *et al.*, Current Protocols in Molecular Biology (1995), John Wiley & Sons, Inc.). --